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Classification of Rice Seedling Structures Using ResNet-50 with Data Augmentation and K-fold Cross Validation

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Abstract *- This study evaluates the efficacy of a Convolutional Neural Network (CNN) with ResNet-50 architecture for classifying rice seedling structures into three categories: normal sprouts, abnormal sprouts, and dead seeds. A dataset of 400 images was collected from the Seed Science and Plant Breeding Laboratory, augmented to 1600 images using horizontal flip, pad-crop, and rotation techniques. The model was trained using the Adam optimizer (learning rate=0.001) over 10 epochs and validated with 10-fold cross-validation. Results demonstrated significant accuracy improvements; the baseline model achieved 82.50% accuracy, while the augmented model reached 93.75%. Incorporating k-fold cross-validation further enhanced performance to 92.25% (no augmentation) and 99.67% (with augmentation). These findings underscore the importance of data augmentation in reducing overfitting and improving generalization for image classification.*

Keywords**:** *Convolutional Neural Network; Data Augmentation; K-Fold Cross Validation; ResNet-50; Rice Seedlings.*

1. INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most vital crops for global food security, feeding more than half of the world's population [1]. The success of rice cultivation depends on seed quality, which directly influences crop yields and agricultural sustainability. Accurate classification of seedling structures, such as healthy sprouts, malformed sprouts, and non-germinating seeds, is essential for optimizing seed selection and improving farming outcomes. Traditional evaluation methods, such as those outlined in the ISTA Handbook for Seedling Evaluation, rely heavily on manual inspections by trained experts [2]. Although these protocols are standardized, they are time-consuming and susceptible to subjective bias when applied to large-scale datasets. These challenges underscore the urgent need for automated solutions capable of delivering consistent, objective, and scalable assessments of seed quality.

In recent years, deep learning, particularly convolutional neural network (CNN), has revolutionized agricultural research by extracting intricate patterns from visual data and enabling accurate image classification. ResNet-50, a CNN architecture distinguished by its residual learning mechanism, effectively mitigates the vanishing-gradient problem, allowing much deeper network to extract complex features from agricultural imagery (e.g., seedling structures, plant leaves, and weeds) without losing fundamental information [3]. This architecture also leverages transfer learning from ImageNet-pre trained weights, facilitating adaptation to agricultural datasets that are often small or imbalanced while maintaining strong performance on tasks such as plant-disease classification [4-5]. Various empirical studies have reported accuracies of up to 98-99% in plant-leaf disease classification and weed detection, outperforming or matching other state-of-the-art architectures in agricultural domain [6-7]. Despite its promise, ResNet-50's application to nuanced seedling-health classification remains underexplored. For example, Nguyen et al. [8] developed a vision-based method for automatic evaluation of rice seed germination rates, reporting F1 scores of 93.38% for segmentation and 95.66% for classification without employing ResNet-50.

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Similarly, Koklu et al. [9] classified rice varieties using CNN and achieving 100% accuracy but not utilizing deeper residual network such as ResNet-50. However, neither study investigated the ability of the ResNet-50 architecture to differentiate subtle structural anomalies in seedlings, such as stunted roots or irregular shoot development. A gap that limits the practical application of deep learning in early seed quality assessment.

In this study, we systematically evaluate ResNet-50's classification performance on rice seedling images under two experimental conditions [10]. First, we train a baseline model using 400original RGB images of rice seedlings [11]. Second, we construct an augmented dataset by applying horizontal flipping, padding-cropping, and rotation to expand the original 400 images into 1600 samples [12]. To ensure robustness and prevent overfitting, we employ 10-fold cross-validation, partitioning the data into ten subsets for iterative training and validation [13].

This validation strategy enhances the model's generalizability to unseen data, a critical requirement in agricultural applications with limited labelled datasets [14]. By isolating the effect of data augmentation and cross-validation, we quantify how specific augmentation techniques contribute to performance improvements [15]. We observe that the augmented ResNet-50 model achieves significantly higher accuracy and F1-scores compared to the baseline [16].

Our results provide practical for selecting augmentation parameters, such as rotation angles and crop sizes, when working with small-scale plant phenotyping datasets. This experiment framework offers a reproducible workflow for researchers aiming to optimize deep architectures in precision agriculture. To our knowledge, this study represents one of the first peer-reviewed evaluations of ResNet-50 performance with controlled augmentation and rigorous cross-validation in the context of early-stage seedling health assessment.

2. RESEARCH METHODOLOGY

This study employs a comprehensive framework comprising data acquisition, augmentation, dataset partitioning, deep learning architecture design, and evaluation metrics to categorize rice seedling structure into three distinct classes: normal sprouts, abnormal sprouts, and nonviable seeds [2]. The experimental, depicted in Figure 1, systematically progresses from data preprocessing to performance assessment.

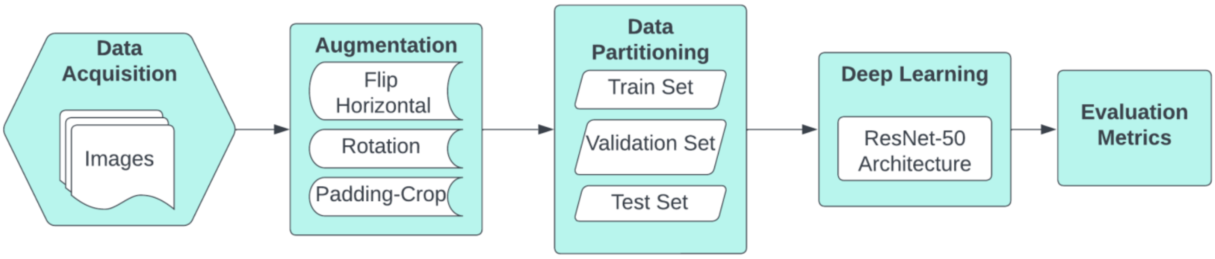

Figure 1. Research methodology.

2.1. Data Collection and Augmentation

Image data of rice seedling structures were collected from the Seed and Plant Breeding Laboratory at the University of Lampung. The dataset comprises three classes (normal sprouts, abnormal sprouts, and dead seeds), defined using morphological criteria outlined in the Handbook for Seedling Evaluation published by the International Seed Testing Association (ISTA).

To enhance data diversity and model robustness, augmentation techniques were applied: horizontal flip, padding-crop, and rotation. These methods generate modified versions of original images, ensuring the model recognizes variations as identical entities (Table 2). Post-augmentation, the dataset expanded to 1600 images, with class distributions detailed in Table 1.

Table 1. Dataset distribution.

Class	Original Dataset	Augmented Dataset
Normal sprouts	150	600
Abnormal sprouts	150	600
Dead seeds	100	400
Total	**400**	**1600**

Table 2. Augmentation examples.

Original	Horizontal Flip	Padding-Crop	Rotation
			

2.2. Data Partitioning

The rice seedling image dataset is partitioned into three subsets: a training set (70%), a validation set (10%), and a test set (20%). This distribution aligns with conventional practices in image classification research to optimize model training while maintaining robust evaluation procedures [17].

In the k-fold cross validation strategy, the dataset is systematically partitioned according to the specified k-value. The validation phase employed 10-fold cross validation, where the training data were partitioned into 10 equally sized folds, with each iteration training the model on 9/10 of the data and utilizing the remaining 1/10 to evaluate validation performance. The use of 10-fold cross validation is recommended because it balances low bias and controlled variance [18-20].

2.3. Model Architecture and Training

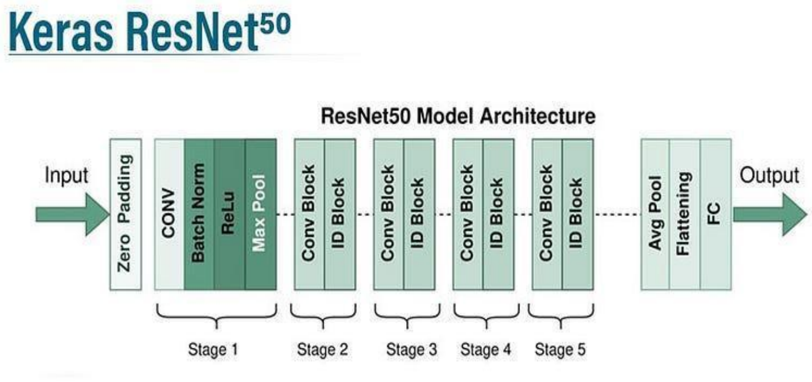

Figure 2. ResNet-50 architecture.

The ResNet-50 architecture, depicted in Figure 2, was adapted for this study. The model begins with zero-padding and convolutional layers for feature extraction, followed by batch normalization and ReLU activation. Four subsequent stages utilize residual blocks with skip connections to address vanishing gradients [21]. Modifications included a Global Average Pooling 2D layer to reduce spatial dimensions and a dense layer with softmax activation for three-class classification. These adjustments align with transfer learning strategies for domain-specific tasks [22].

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2.4. Performance Evaluation

Model performance was assessed using accuracy, precision, recall, and F1-score (Equations 1-4). Accuracy measures overall prediction correctness, while precision and recall evaluate class-specific performance, critical for addressing class imbalances [23]. The F1-score harmonizes these metrics, providing a balanced evaluation for multiclass scenarios. Results were validated against test data to ensure generalizability. This methodology synthesizes established practices in deep learning and agricultural image analysis, ensuring reproducibility and alignment with prior work in convolutional neural networks [24].

Accuracy quantifies the model’s overall prediction correctness by comparing its outputs against the ground-truth labels in the testing dataset. It is computed using Equation (1) as the ratio of accurately classified instances (correctly identified as positive or negative) to the total number of instances evaluated. The denominator represents the total number of seeds in the testing set, while the numerator reflects the number of seeds correctly identified as positive or negative.

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \tag{1}$$

Precision measures the reliability of positive predictions by determining how many identified positives are genuine. As defined in Equation (2), precision is calculated by dividing true positives (TP) by all instances predicted as positive (TP+FP). A high precision value minimizes FP cases, where non-target samples are incorrectly labeled as positive.

$$\text{Precision} = \frac{TP}{TP+FP} \tag{2}$$

Recall evaluates the model’s ability to detect all relevant positive instances within the testing set. Using Equation (3), recall is the proportion of true positives relative to the sum of true positives and overlooked positives (false negatives). A low recall suggests the model frequently misses true positives, misclassifying them as negative.

$$\text{Recall} = \frac{TP}{TP + FN} \tag{3}$$

F1-score harmonizes precision and recall into unified metric, addressing scenarios where optimizing one metric might compromise the other. As shown in Equation (4), it is the harmonic mean of precision and recall.

$$\text{F1-score} = 2x\,\frac{Precision\ x\ Recall}{Precision + Recall} \tag{4}$$

This metric is particularly critical for imbalanced datasets, ensuring neither precision nor recall disproportionately dominates performance assessment when evaluated on the testing set.

3. RESULTS AND DISCUSSION

The research focused on classifying rice seedling structures using the ResNet-50 architecture. The dataset was preprocessed to ensure uniformity, with all images resized to 224x224 pixels to fit the model’s input requirements. A batch size of 32 was applied to optimize training speed and reduce memory usage. The dataset comprised three classes: normal sprouts, abnormal sprouts, and dead seeds. The images were stored in variable X, and their corresponding labels were stored in variable y. The model was trained with a learning rate of 0.001, optimized using the Adam Optimizer, and run for 10 epochs.

Figure 3 illustrates the loss and accuracy curves for the model trained without augmentation. The graph shows that the model began to stabilize after the 4th epoch, with a gradual reduction in training loss from the 5th to 7th epoch. By the 8th to the 10th epoch, the model demonstrated consistent performance, with a steady decrease in validation loss, indicating improved generalization on unseen data.

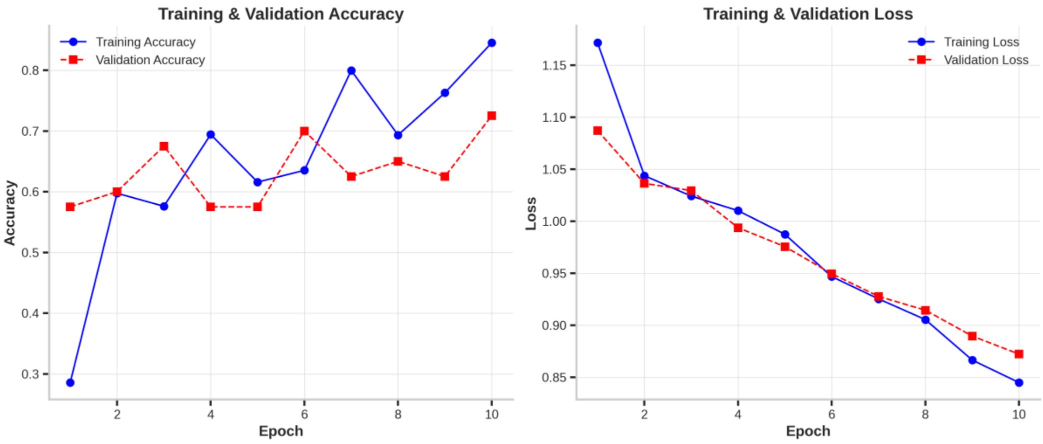

Figure 3. Training and validation accuracy and loss without augmentation.

In contrast, Figure 4 depicts the loss and accuracy curves for the augmented model. The graph shows a significant improvement in performance, with training accuracy increasing from 37.21% in the 1st epoch to 88.57% by the 10th epoch. Validation accuracy also improved the model's ability to recognize patterns in rice seedling structures, leading to better generalization.

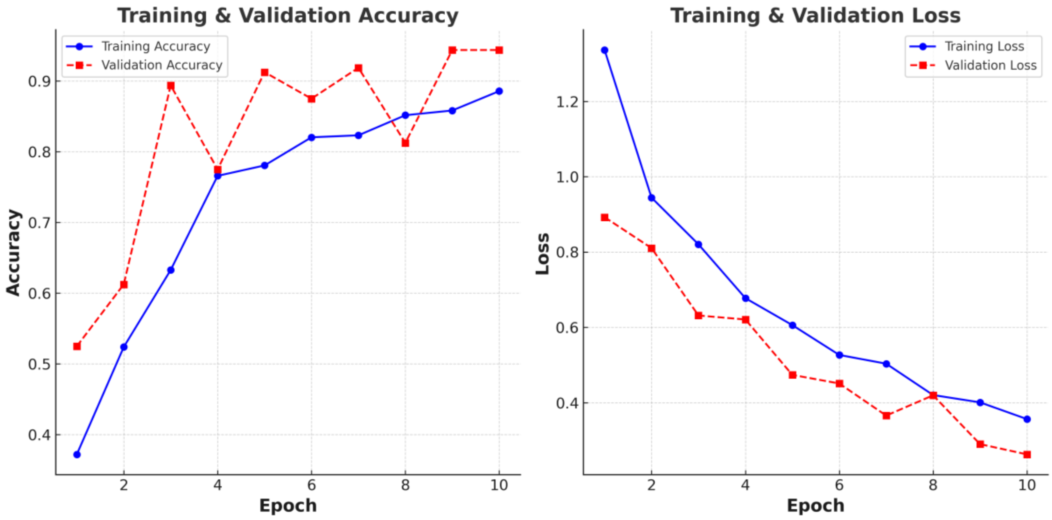

Figure 4. Training and validation accuracy and loss with augmentation.

Table 3 compares the classification results of the model trained without augmentation and the model trained with augmentation. The model without augmentation achieved an accuracy of 82.50% using a dataset of 400 images, while the model with augmentation achieved a significantly higher accuracy of 93.75% using a larger dataset of 1600 images. The training time for the augmented model was 4.1 minutes, compared to 1 minute for the non-augmented model. This indicates that while data augmentation increases computational time, it significantly improves model performance.

Table 3. Performance comparison of ResNet-50 model with and without augmentation.

ResNet-50 Architecture	Dataset Size	Accuracy	Training Time
Without augmentation	400	82.50%	1 minute
With augmentation	1600	93.75%	4.1 minutes

Figure 5 shows the accuracy and loss curves for the non-augmented model using k-fold cross-validation. The graph reveals variability in performance across folds, with Fold 8 achieving the highest accuracy of 100%, while Folds 1 and 2 showed the lowest accuracy of 82.50%**.** Despite this variability, the model demonstrated a consistent upward trend in accuracy, indicating effective learning across different data subsets.

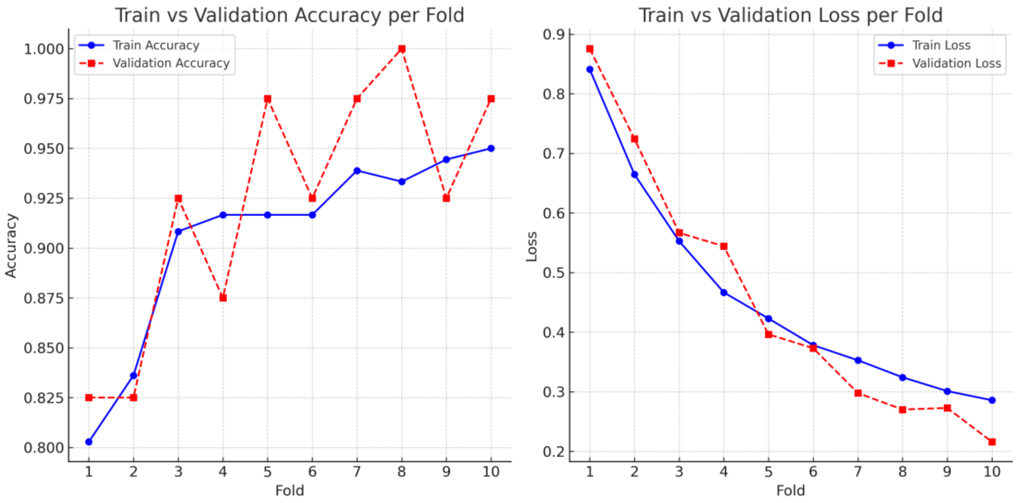

Figure 5. K-Fold cross validation accuracy and loss without augmentation.

Figure 6 illustrates the accuracy and loss curves for the augmented model using k-fold cross-validation. The graph shows a remarkable improvement in performance, with training accuracy reaching 98.28% in the 1st fold and consistently increasing to 100% by the 10th fold. This indicates that the augmented model achieved near-perfect accuracy across all folds, demonstrating its robustness and generalization capabilities.

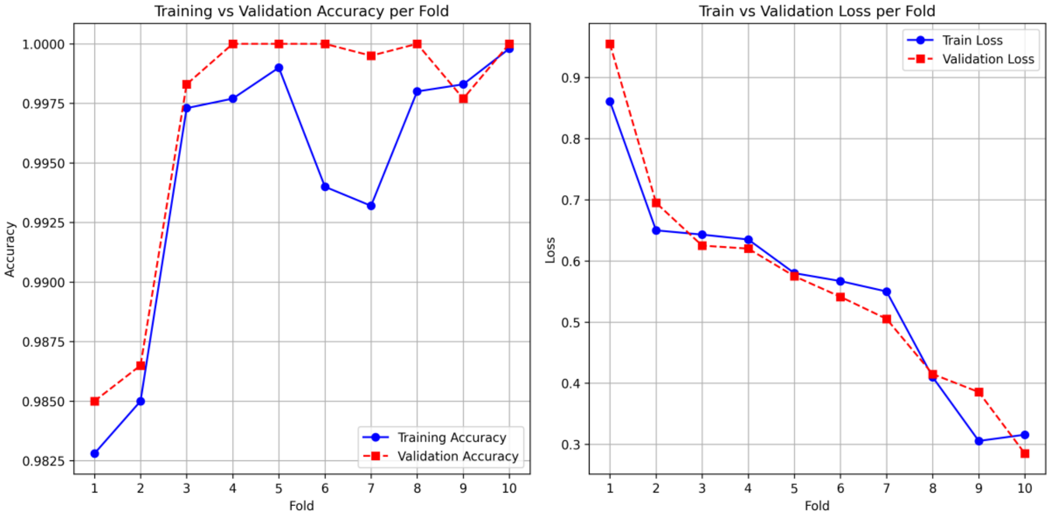

Figure 6. K-Fold cross validation accuracy and loss with augmentation.

Table 4 provides the accuracy for each fold in the non-augmented model, with an overall accuracy of 92.25%. The highest accuracy was observed in Fold 8, while the lowest was in Folds 1 and 2.

Table 4. K-Fold cross validation accuracy without augmentation.

K-Fold Cross Validation	Accuracy
Fold-1	82.50%
Fold-2	82.50%
Fold-3	92.50%

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K-Fold Cross Validation	Accuracy
Fold-4	87.50%
Fold-5	97.50%
Fold-6	92.50%
Fold-7	97.50%
Fold-8	100%
Fold-9	92.50%
Fold-10	97.50%
Total Accuracy	**92.25%**

Table 5 provides the accuracy for each fold in the augmented model, with an overall accuracy of 99.67%. Five out ten folds (Fold-4 to Fold-8 and Fold-10) achieved perfect 100% accuracy, while the remaining folds (Fold-1: 98.50%, Fold-2: 98.65%, Fold-3: 99.83%, Fold-9: 99.77%) demonstrated near-perfect performance. The total accuracy of 99.67% underscores the robustness of combining k-fold cross validation with data augmentation, as the model consistently delivered results across almost all folds.

Table 5. K-Fold cross validation accuracy with augmentation.

K-Fold Cross Validation	Accuracy
Fold-1	98.50%
Fold-2	98.65%
Fold-3	99.83%
Fold-4	100%
Fold-5	100%
Fold-6	100%
Fold-7	100%
Fold-8	100%
Fold-9	99.77%
Fold-10	100%
Total Accuracy	**99.67%**

Table 6 compares the results of the model trained without augmentation and the model trained with augmentation using k-fold cross validation. The non-augmented model achieved an accuracy of 92.25%, while the augmented model achieved an exceptional accuracy of 99.67%. The training time for the augmented model was 6.8 minutes, compared to 2.3 minutes for the non-augmented model. This further confirms the benefits of data augmentation in improving model accuracy, albeit at the cost of increased computational time.

Table 6. Performance comparison of ResNet-50 model using K-Fold cross validation with & without augmentation.

ResNet-50 Architecture	Dataset Size	Accuracy	Training Time
K-Fold cross validation without augmentation	400	92.25%	2.3 minutes
K-Fold cross validation with augmentation	1600	99.67%	6.8 minutes

Figure 7 presents the confusion matrix for the non-augmented model. The matrix shows that the model correctly classified 14 dead seeds, 22 abnormal sprouts, and 30 normal sprouts. However, there were misclassifications, particularly between dead seeds and abnormal sprouts, as well as between abnormal and normal sprouts. Table 7 provides the classification report for the non-augmented model, showing a precision of 93.33% for dead seeds, 78.57% for abnormal sprouts, and 81.08% for normal sprouts. The recall values were 70.00%, 73.33%, and 100%, respectively, with an overall accuracy of 82.50%.

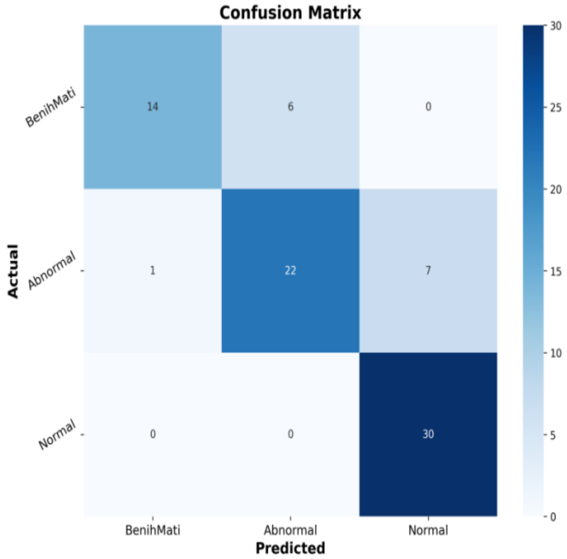

Figure 7. Confusion matrix for model without augmentation.

Table 7. Classification report for model without augmentation

Categories	Results			Support
	Precision	Recall	F1-Score	
Dead Seeds	93.33%	70.00%	80.00%	20
Abnormal Sprouts	78.57%	73.33%	75.86%	30
Normal Sprouts	81.08%	100%	89.55%	30
Accuracy	82.50%			80

In contrast, Figure 8 presents the confusion matrix for the augmented model. The matrix shows significantly improved classification, with 79 dead seeds, 107 abnormal, and 114 normal sprouts correctly classified. Misclassifications were minimal, indicating the model's ability to distinguish between classes.

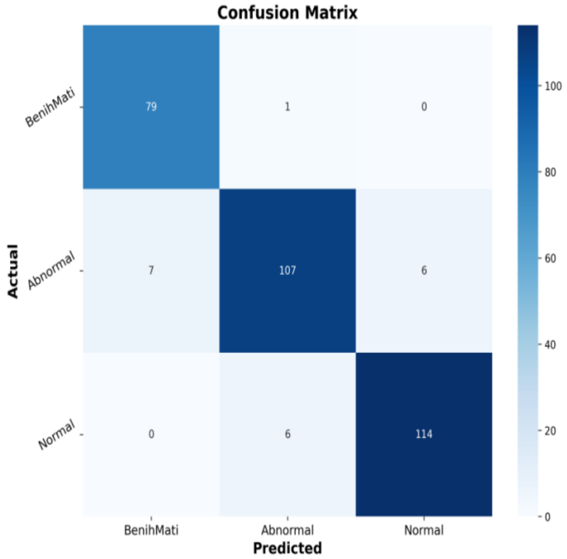

Figure 8. Confusion matrix for model with augmentation.

Table 8 provides the classification report for the augmented model, showing a precision of 91.86% for dead seeds, 93.86% for abnormal sprouts, and 95.00% for normal sprouts. The recall values were 98.75%, 89.17%, and 95.00%, respectively, with an overall accuracy of 93.75%.

Table 8. Classification report for model with augmentation.

Categories	**Results**			**Support**
	Precision	**Recall**	**F1-Score**	
Dead seeds	91.86%	98.75%	95.18%	80
Abnormal sprouts	93.86%	89.17%	91.45%	120
Normal sprouts	95.00%	95.00%	95.00%	120
Accuracy	93.75%			320

Table 9 summarizes the accuracy and training time for all models. It is important to note that the ResNet-50 architecture and hyper-parameter were kept consistent across all experiments to ensure a fair comparison. The highest accuracy of 99.67% was achieved by the model using k-fold cross-validation with augmentation, while the lowest accuracy of 82.50% was observed in the model trained without augmentation. The augmented models consistently outperformed their non-augmented counterparts, demonstrating the importance of data augmentation in improving model generalization and accuracy.

Table 9. Performance comparison of ResNet-50 model.

ResNet-50 Architecture	**Accuracy**	**Training Time**
Without augmentation	82.50%	1 minute
K-Fold cross validation without augmentation	92.25%	2.3 minutes
With augmentation	93.75%	4.1 minutes
K-Fold cross validation with augmentation	99.67%	6.8 minutes

The use of data augmentation techniques (including horizontal flip, padding-crop, and rotation), significantly enhanced dataset diversity by simulating real-world variations in rice seedling morphology, such as natural asymmetries in sprout growth and irregular field angles observed in agricultural settings. This compelled the model to learn invariant features, improving classification accuracy by 7–11% for fine-grained tasks like distinguishing abnormal sprouts from dead seeds. K-fold cross-validation (K= 10) further improved robustness through iterative training and validation on diverse data subsets, reducing bias inherent in single splits and elevating baseline accuracy from 82.50% to 92.25%. When combined with augmentation, the synergy of synthetic and natural variations increased accuracy to 99.67%, as demonstrated in recent agricultural AI research [25-26]. These findings align with advancements in plant phenotyping, where augmentation and k-fold validation address class imbalance (see Table 1, dead seeds are underrepresented) and enhance field applicability.

4. CONCLUSIONS

In conclusion, the results demonstrate that data augmentation and k-fold cross-validation are essential techniques for enhancing the accuracy and generalization capabilities of deep learning models, particularly in image classification tasks. The ResNet-50 architecture, combined with these techniques, proved highly effective in classifying rice seedling structures, achieving near-perfect accuracy in some cases. Future research will focus on developing a model that can be directly applied to germination testing of rice seeds at the Laboratory of Rice Seed Science and Plant Breeding, University of Lampung, employing YOLO or other hybrid approaches for image segmentation and classification.

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